

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 11:04:55 ; Search time 1982 Seconds  
(without alignments)  
6666.907 Million cell updates/sec

Title: US-09-987-899-5

Perfect score: 323

Sequence: 1 cgactgtgtgaagcaggtgg.....ccgcgcgcgcgcgcgcgcgc 323

Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sta.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sv.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	311	96.3	830	8	MZEPCCSSU	D00170 Zea mays mRNA
2	311	96.3	830	8	ZMRUBSSU	X06535 Maize mRNA
3	295	91.3	1648	8	ZMRBBS	Y03122 Maize rbcS
4	271	83.9	1274	8	ZMRUBSSU	Y09114 Z.mays rubi
5	222.6	68.9	2328	8	SCFBCSIA	M86717 Saccharum h
6	201.8	62.5	808	8	RICCPBCLA	L22155 Oryza sativ
7	201.8	62.5	830	8	RICRUBPC1	D00643 Oryza sativ
8	201.8	62.5	14590	8	CNS08C70	AL731739 Oryza sat
9	198.8	61.5	960	6	E06908	E06908 Zoyaia rbes
10	198.6	61.5	854	8	AF017364	AF017364 Oryza sat
11	197	61.0	835	8	AF052305	AF052305 Oryza sat
12	192.2	59.5	591	8	AB020942	AB020942 Secale ce
13	192.2	59.5	604	8	AB020944	AB020944 Agropyron
14	192.2	59.5	787	8	AB020954	AB020954 Triticum
15	192.2	59.5	895	8	RICRUBPC2	D00644 Oryza sativ
16	190.6	59.0	638	8	AB042065	AB042065 Triticum
17	190.6	59.0	781	8	AB020953	AB020953 Aegilops
18	190.6	59.0	787	8	AB020955	AB020955 Triticum
19	190.6	59.0	12767	2	CNS0984U	BX119951 Oryza sat
20	189.6	58.7	845	8	SCB131737	AT117377 Secale ce
21	189	58.5	504	8	AF192776	AF192776 Avena cla
22	189	58.5	504	8	AF192779	AF192779 Avena mar
23	189	58.5	605	8	AB020943	AB020943 Hordeum v
24	189	58.5	611	8	AB020937	AB020937 Aegilops
25	189	58.5	781	8	AB020958	AB020958 Triticum
26	189	58.5	2205	8	WHTRUBIAA	M37328 T.aestivum
27	189	58.5	5980	8	AB042069	AB042069 Triticum
28	188	58.2	789	8	AB020959	AB020959 Secale ce
29	187.4	58.0	600	8	AF202645	AF202645 Avena cla
30	187.4	58.0	604	8	AB020939	AB020939 Triticum
31	187.4	58.0	607	8	AB020938	AB020938 Aegilops
32	187.4	58.0	611	8	TARUB1	X00234 Wheat mRNA
33	187.4	58.0	728	8	AB020952	AB020952 Aegilops
34	187.4	58.0	792	8	AB020949	AB020949 Aegilops
35	187.4	58.0	792	8	AB020950	AB020950 Aegilops
36	187.4	58.0	985	8	AB042068	AB042068 Triticum
37	185.8	57.5	504	8	AF192773	AF192773 Avena aga
38	185.8	57.5	605	8	AB020932	AB020932 Aegilops
39	185.8	57.5	605	8	AB020933	AB020933 Aegilops
40	185.8	57.5	605	8	AB020934	AB020934 Aegilops
41	185.8	57.5	605	8	AB020935	AB020935 Aegilops
42	185.8	57.5	605	8	AB020936	AB020936 Aegilops
43	185.8	57.5	620	8	AF202648	AF202648 Avena mar
44	185.8	57.5	787	8	AB020946	AB020946 Aegilops
45	185.8	57.5	875	8	SCB131738	AJ11738 Secale ce

# ALIGNMENTS

RESULT 1  
MZEPCCSSU  
LOCUS  
DEFINITION Zea mays mRNA for ribulose 1,5-bisphosphate carboxylase small subunit, complete cds.  
830 bp mRNA linear PLN 13-NOV-1997  
ACCESSION D00170  
VERSION D00170.1 GI:217963  
KEYWORDS RuBPC; ribulose-1,5-bisphosphate carboxylase; small subunit.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 830)  
AUTHORS Matsuoka,M., Kano-Murakami,Y., Tanaka,Y., Ozeki,Y. and Yamamoto,N.



REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD									
AUTHORS	Clade; Panicoideae; Andropogoneae; Zea.									
TITLE	1 (bases 1 to 1648)									
	Lebrun, M., Waksman, G. and Freyssonnet, G.									
	Nucleotide sequence of a gene encoding corn									
	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit									
	(rbcs)									
JOURNAL	Nucleic Acids Res. 15 (10), 4360 (1987)									
MEDLINE	87231019									
PUBMED	3588298									
REFERENCE	2 (bases 1 to 1648)									
AUTHORS	Freyssinet, G.									
TITLE	Direct Submission									
JOURNAL	Submitted (16-Oct-1987)									
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source	1..1648									
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CAAT_signal	359..362									
TATA_signal	398..403									
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	/EC number="4.1.1.39"									
	/codon_start=1									
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	/protein_id="CA68419.1"									
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	/db_xref="SWISS-PROT:P05348"									
	/translation="MAPTNMVASATAVAPFQGLKSTASLPVARRSRSLGNTVNSGR									
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	IAYKPGSD"									
exon	491..637									
	/gene="rbcs"									
	/number=1									
misc_feature	631..632									
	/gene="rbcs"									
	/note="pot. site of cleavage of transit peptide"									
intron	638..800									
	/gene="rbcs"									
	/number=1									
exon	801..1160									
	/gene="rbcs"									
	/number=2									
BASE COUNT	368 a 509 c 411 g 360 t									
ORIGIN										
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Best Local Similarity	98.8%; Pred.No. 2.1e-45;									
Matches 319; Conservative	0; Mismatches 0; Indels 4; Gaps 2;									
QY	1	CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTCGCTCCAGTT	60							
Db	866	CGACCTGCTGAAGCAGGTGGACTAC	---	CTGCGCAACGGCTGGATACCTCGCTCCAGTT	922					
QY	61	CAGCAGGTCCGGCTTCGTGTACGCGAGAACTCCACTCCCGCTGCTACTACGACGGCCG	120							
Db	923	CAGCAAGGTCCGGCTTCGTGTACGCGAGAACTCCACTCCCGCTGCTACTACGACGGCCG	982							
QY	121	CTACTGACCATGTGGAAGCATGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA	180							
Db	983	CTACTGACCATGTGGAAGC	-TGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA	1041						
QY	181	AGGAGTGTGAGGAGGCCATCAAAATCTCTACCCGACGCGCTTCCACCGGCTCATCGGCTTCG	240							
Db	1042	AGGAGTGTGAGGAGGCCATCAAAATCTCTACCCGACGCGCTTCCACCGGCTCATCGGCTTCG	1101							
QY	241	ACAACATCAGCAGACGCGAGTGGCTCAGCTTCATCGCTTCAATCGCCTTCAAGCGCCCGGAGCGACT	300							

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QY 241 ACAACATCAAGCAGACGCGAGTGGTTCAGCTTTCATCGCTTACAGCCCGCGGCGGAGCT 300
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Db 765 ACAACGTCAGGACGACGAGTGGTTCAGCTTTCATCGCTTACAGCCCGCGGCGGAGCT 824
|||
QY 301 AGACCGCGCGCGCGCGCGCGCG 323
|||
Db 825 AGAGACCGTGGCTAGATCGACCC 847
|||

RESULT 5
SCREBS1A 2328 bp DNA linear PLN 16-JUN-1999
LOCUS Saccharum hybrid cultivar H32-8560 ribulose 1,5-bisphosphate
DEFINITION carboxylase/oxygenase small subunit gene, complete cds.
ACCESSION M86717
VERSION M86717.1 GI:169841
KEYWORDS Saccharum hybrid cultivar H32-8560
SOURCE Saccharum hybrid cultivar H32-8560
ORGANISM Saccharum hybrid cultivar H32-8560
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 2328)
Tang,W. and Sun,S.S.
Sequence of a sugarcane ribulose-1,5-bisphosphate
carboxylase/oxygenase small subunit gene
plant Mol. Biol. 21 (5), 949-951 (1993)
JOURNAL 93222494
MEDLINE
PUBMED 8467089
FEATURES
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Location/Qualifiers
1..2328
/organism="Saccharum hybrid cultivar H32-8560"
/mol_type="genomic DNA"
/cultivar="H32-8560"
/db_xref="taxon:50502"
1066..1071
TATA_signal
CDS
join(1172..1315,1411..1773)
/notes="ORF"
/codon_start=1
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small subunit"
/protein_id="AAA33922.1"
/db_xref="GI:169842"
/translation="MALTMVSSATAAAPQGLKSTASLPVARRSTSLAKVNGGRI
RCMQVMPAYGNKKFTLSYLPLOTQQLKQVDYLLRNWVPCLEFSKGFVYRENT
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AVKPAGSE"
1172..1309
sig_peptide
mat_peptide
join(1310..1315,1411..1770)
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small subunit"
1172..1315
exon
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1316..1410
intron
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1411..>1773
exon
/number=2
BASE COUNT 539 a 679 c 578 g 532 t
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Query Match 68.9%; Score 222.6; DB 8; Length 2328;
Best Local Similarity 87.5%; Pred. No. 6.3e-32;
Matches 267; Conservative 0; Mismatches 34; Indels 4; Gaps 2;

QY 3 ACCTGCTGAACGAGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTTCA 62
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Db 1478 AGCTGCTGAACGAGTGGACTACCTGCTGCGCAACACTGGTCCCTGCTCGAGTTCA 1537
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QY 63 GCAAGGTGGTTCGTGTACCGCAGAACTCCACCTCCCGTGTCTACTACAGCGCGCT 122
|||
Db 1538 GCAAGGAAGGCTTGTGTACCGCAGAACTCCACCTCCCGTGTCTACTACAGCGCGGT 1597
|||

QY 123 ACTGACCATGGAAGCATGCCATGTTTCGGCTGCAACGACGCCACCCAGCGTGTACAAG 182
|||
Db 1598 ACTGACCATGGAAGC-TGCCCATGTTTCGGCTGCAACGACGCCAGCGTGTACAAG 1656
|||
QY 183 GAGCTGCAGGAGGCATCAAAATCTTACCCGAGCGCTTCCACCGGTTTCATCGCTTCGAC 242
|||
Db 1657 GAGCTGCAGGAGGCATCGCTCTTACCCGGA--GCTACGTGTCATCTCGGCTTCGAC 1713
|||
QY 243 AACATCAAGCAGACGCGTGGTTCAGCTTTCATCGCTTACAGCCCGCGGCGGAGCTAG 302
|||
Db 1714 AACATCAAGCAGACGCGTGGTTCAGCTTTCATCGCTTACAGCCCGCGGCGGAGCTAA 1773
|||
QY 303 ACCGC 307
|||
Db 1774 AGTGC 1778
|||

RESULT 6
RCCPRBCLA 808 bp mRNA linear PLN 21-DEC-1995
LOCUS Oryza sativum mitochondrial ribulose bisphosphate
DEFINITION carboxylase/oxygenase (rbcS) mRNA, complete cds.
ACCESSION L22155
VERSION L22155.1 GI:347450
KEYWORDS ribulose bisphosphate carboxylase/oxygenase.
SOURCE chloroplast Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 808)
Moon,E.P., Lee,K.W., Lee,J.S., Choi,Y.D. and Kim,H.J.
Isolation and Characterization of cDNAs for Ribulose Bisphosphate
Carboxylase Multigene Family in Rice (Oryza)
Mol. Cells 1, 287-294 (1991)
JOURNAL
COMMENT Original source text: Chloroplast Oryza sativa leaf etiolated cDNA
to mRNA.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:4530"
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1..808
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53..562
CDS
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bisphosphate"
/notes="putative"
/codon_start=1
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/protein_id="AAA84592.1"
/db_xref="GI:347451"
/translation="NASSATTVPFQGLKSTAGMPVARRSNSSFGVNSGGRIRCMQV
WPQIKKPTLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKGVYRENNHKSPPGY
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PGCESGGN"
polyA_site
808
BASE COUNT 159 a 226 c 220 g 203 t
ORIGIN
Query Match 62.5%; Score 201.8; DB 8; Length 808;
Best Local Similarity 81.0%; Pred. No. 5.2e-28;
Matches 247; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

QY 2 GACCTCTGAACGAGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTTTC 61
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Db 248 GACCTCTGAACGAGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTTTC 307
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QY 62 AGCAAGGTGGCTTGTGTACCGGAGAACTCCACCTCCCGCTGCTACTACGACGGCGC 121
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Db 308 AGCAAGGTGGGATTGTCTACCTGAGAACCAAGTCCCGCTGGATACTACGACGGCAGG 367
|||||
QY 122 TACTGGACCATGTGGAAGCATGCCATGTTCCGCTGCACGACGCCACCGAGGTGTACAA 181
|||||
Db 368 TACTGGACCATGTGGAAGC-TGCCCATGTTCCGGGTGACCGACGCCACCGAGGTGTCAA 426
|||||
QY 182 GGAGCTGCGAGGAGCCATCAAAATCCTACCGGACGGCTTCCACCGGGTTCATCGGCTTCCA 241
|||||
Db 427 GGAGCTGCGAGGAGGCCAAGAAGCGTACCTGATGATTCGTCGTATCATCGCTTCCA 486
|||||
QY 242 CAACATCAAGCAGCAGTGGCTGAGCTTCAGCTTCATCGCTCAAGACCCCGGGGACGCACTA 301
|||||
Db 487 CAACGTTAGCGAGGTGAGCTCATCAGCTTCATCGCTCAAGACCCCGGGGTCGAGGA 546
|||||
QY 302 GACCG 306
Db 547 GTCTG 551

RESULT 7
LOCUS RICRUBPC1
DEFINITION Oryza sativa (japonica cultivar-group) mRNA for the small subunit
of ribulose-1,5-bisphosphate carboxylase, complete cds, clone
POSS81139.
ACCESSION D00643 M36715
VERSION D00643.1 GI:218207
KEYWORDS RuBPC; ribulose-1,5-bisphosphate carboxylase; small subunit.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 830)
AUTHORS Matsuoka,M., Kano-Murakami,Y., Tanaka,Y., Ozeki,Y. and Yamamoto,N.
TITLE Classification and nucleotide sequence of cDNA encoding the small
subunit of ribulose-1,5-bisphosphate carboxylase from rice
JOURNAL Plant Cell Physiol. 29, 1015-1022 (1988)
COMMENT These data kindly submitted in computer readable form by: Makoto
Matsuoka
National Institute of Agrobiological Resources
Tsukuba Science City
Ibaraki 305
Japan
Phone: 0298-38-8381
Fax: 0298-38-8199.
Location/Qualifiers
1. .830
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="POSS81139"
55. .582
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carboxylase (RuBPC)"
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BASE COUNT 167 a 233 c 222 g 208 t
ORIGIN
Query Match 62.5%; Score 201.8; DB 8; Length 830;
Best Local Similarity 81.0%; Pred. No. 5.2e-28;
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Matches 247; Conservative 0; Mismatches 57; Indels 1; Gaps 1;
QY 2 GACCTCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTCCTCGAGTTC 61
|||||
Db 268 GACCTCTGAAGCAGATCGAGTACCTGCTCCGTTCCAGTGGGTGCTCGAGTTC 327
|||||
QY 62 AGCAAGGTGGCTTGTGTACCGGAGAACTCCACCTCCCGCTGCTACTACGACGGCGC 121
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Db 328 AGCAAGGTGGGATTGTCTACCGTGAGAACCAAGATCCCGGATACTACGATGGCAGG 387
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QY 122 TACTGGACCATGTGGAAGCATGCCATGTTCCGCTGCACGACGCCACCGAGGTGTACAA 181
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Db 388 TACTGGACCATGTGGAAGC-TGCCCATGTTCCGGGTGACCTGACGACCCCGAGGTGTCAA 446
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QY 182 GGAGCTGCGAGGAGCCATCAAAATCCTACCGGACGGCTTCCACCGGGTTCATCGGCTTCCA 241
|||||
Db 447 GGAGCTGCGAGGAGGCCAAGAAGCGTACCTGATGATTCGTCGTATCATCGCTTCCA 506
|||||
QY 242 CAACATCAAGCAGCAGTGGCTGAGCTTCAGCTTCATCGCTCAAGACCCCGGGGACGACTA 301
|||||
Db 507 CAACGTCAGGCAGGTGAGCTCATCAGCTTCATCGCTCAAGACCCCGGGGTCGAGGA 566
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QY 302 GACCG 306
Db 567 GTCTG 571

RESULT 8
LOCUS CNS08C70
DEFINITION Oryza sativa chromosome 12, . BAC OSJNBa0056118 of library OSJNBa
from chromosome 12 of cultivar Nipponbare of ssp. japonica of Oryza
sativa (rice), complete sequence.
ACCESSION AL731739
VERSION AL731739.3 GI:27552306
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 145890)
AUTHORS Choisne,N., Orjeda,G., Cattolico,L., Demange,N., Wincker,P.,
Segurens,B., Pelletier,E., Scarpelli,C., Salanoubat,M.,
Weissenbach,J. and Quetier,F.
TITLE Oryza sativa chromosome 12 sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 145890)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Jan 9, 2003 this sequence version replaced gi:25956054.
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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The following sequence is oriented from the T7 to the SP6 end.
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FINISHED SEGMENT ENDS AT BASE 145890
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/chromosome="12"
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FEATURES
source
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Best Local Similarity		81.0%; Pred. No. 3.3e-28;			
Matches		247; Conservative 0; Mismatches 57; Indels 1; Gaps 1;			
QY	2	GACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTTTC	61		
Db	82537	GACCTCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTTTC	61		
QY	62	AGCAAGGTGGCTTGTGTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCCGC	121		
Db	82597	AGCAAGGTGGCTTGTGTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCCGC	121		
QY	122	TACTGGACCATGTGGAAGCATGCCATGTTGGCTGCAACGCGCCACCGAGTGTACAA	181		
Db	82657	TACTGGACCATGTGGAAGCATGCCATGTTGGCTGCAACGCGCCACCGAGTGTACAA	181		
QY	182	GGAGCTGCGAGGAGCCATCAATCTTCCCGGAGCGCTTCCACCGCGTTCATCGGTTTCA	241		
Db	82716	GGAGCTGCGAGGAGCCATCAATCTTCCCGGAGCGCTTCCACCGCGTTCATCGGTTTCA	241		
QY	242	CAACATCAAGCAGCAGTGTGCTGCTGCTGCAACGCGCCACCGAGTGTACAA	301		
Db	82776	CAACATCAAGCAGCAGTGTGCTGCTGCTGCAACGCGCCACCGAGTGTACAA	301		
QY	302	GACCG 306			
Db	82836	GTCTG 82840			
RESULT 9		E06908			
LOCUS		E06908			
DEFINITION		Zoisia rhes gene.			
ACCESSION		E06908.1 GI:2175064			
VERSION		JP 1994070781-A/1.			
KEYWORDS		unidentified			
SOURCE		unclassified.			
ORGANISM		1 (bases 1 to 960)			
REFERENCE		Uchida,E.			
AUTHORS		INDUCTION OF GENE MANIFESTATION			
TITLE		Patent: JP 1994070781-A 1 15-MAR-1994;			
JOURNAL		JAPAN TAAFU GLASS:KK			
COMMENT		OS Zoisia			
		PN JP 1994070781-A/1			
		PD 15-MAR-1994			
		PF 20-JUN-1991 JP 1991174806			
		PI UCHIDA ETSUKO			
		PC C12N15/82,A01H1/00//C12N5/10,(C12N5/10,C12R1:91); CC			
		strandedness: Double;			
		CC topology: Linear;			
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		FT TATA_signal 88..94			
		FT CDS 341..829			
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Db	592	AGCAAGGTGGCTTGTGTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCCGC	651
QY	122	TACTGGACCATGTGGAAGCATGCCATGTTGGCTGCAACGACGCCACCGAGTGTACAA	181
Db	652	TACTGGACCATGTGGAAGC-TCCCATGTTTCGGTGCACCGACGCCACTCAGGTGCTCAA	710
QY	182	GGAGCTGCGAGGAGCCATCAATCTTCCCGGAGCGCTTCCACCGCGTTCATCGGCTTCGA	241
Db	711	GGAGATGAGGAGTGCAGAGGGGCTACCCCGATGCTTTCATCCGCGTTCATCGGCTTCGA	770
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QY	302	GACCGCGCCC 311	
Db	831	AGCGAGCTC 840	
RESULT 10		AF017364	
LOCUS		AF017364	
DEFINITION		Oriza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds.	
ACCESSION		AF017364	
VERSION		AF017364.1 GI:2407282	
KEYWORDS		Oriza sativa (indica cultivar-group)	
SOURCE		Oriza sativa (indica cultivar-group)	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oriza.	
REFERENCE		1 (bases 1 to 854)	
AUTHORS		Lee,M.C., Kim,C.S. and Eun,M.Y.	
TITLE		Characterization of Ribulose 1,5-bisphosphate carboxylase small subunit from rice	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 854)	
AUTHORS		Lee,M.C., Kim,C.S. and Eun,M.Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (07-AUG-1997) CytoGenetics, International Institute of Agricultural Science and Technology, Sedun-Dong, RDA, Suwon 441-707, Korea	
FEATURES		Location/Qualifiers	
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		/clone="KCDM2416"	
		/dev_stage="immature seed (milky stage)"	
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		/codon_start=1	
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BASE COUNT		173 a 239 c 230 g 212 t	
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Query Match	61.5%;	Score 198.6;	DB 8;	Length 854;
Best Local Similarity	80.3%;	Pred. No. 2e-27;		
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Qy	182	GGAGCTCGAGGAGGCCATCAATCTCTACCGGACGCCTTCCACCGCGTCATCGGCTTCGA	241	
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Db	595	GTCTG	599	

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DEFINITION	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds.
ACCESSION	AF052305
VERSION	AF052305.1 GI:3063523
KEYWORDS	.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1 (bases 1 to 835)
AUTHORS	Yoon,U.H., Hahn,J.H., Yun,C.-H. and Eun,M.Y.
TITLE	Molecular cloning and characterization of cDNA encoding the small subunit of ribulose 1,5-bisphosphate carboxylase in rice
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 835)
AUTHORS	Yoon,U.H., Hahn,J.H., Yun,C.-H. and Eun,M.Y.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAR-1998) Cytogenetics, National Institute of Agricultural Science and Technology, Seodun-dong, Suwon 441-707, Korea

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BASE COUNT	187 a	226 c 201 t

[illegible]

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RESULT 12
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LOCUS
DEFINITION
AB020942
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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Best Local Similarity 80.1%; Pred. No. 3.3e-26;
Matches 238; Conservative 0; Mismatches 58; Indels 1; Gaps 1;
QY 2 GACCTCTGAAGCAGGTGGACTACCTGCTGCGCAACGGTGGATACCCCTGCTCGAGTTC 61
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QY 62 AGCAAGTTCGGCTTCGTGACCGGAGAACTCCACCTCCCGTGTACTACGACGGCCGC 121
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DB 413 TACTGACCATGTGGAAGC-TGCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACAA 471
QY 182 GGAGCTGCGAGGAGCCATCAATTCCTACCGGACGGCTTCCACCGGTCATCGGCTTCCA 241
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QY 242 CACATCAGCAGCAGCGTGCCTGAGCTTCATCGCTCAAGCCCGCGGACGCA 298
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RESULT 13
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DEFINITION
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carboxylase/oxygenase small subunit, partial cds, clone Agr-A.
AB020944
ACCESSION
AB020944.1 GI:4038692
VERSION
Small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase.
Thiopyrum intermedium
SOURCE
Thiopyrum intermedium
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Thinopyrum.
REFERENCE
1 (sites)
Sasanuma,T. and Miyashita,N.T.
Subfamily divergence in the multigene family of
ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) in Triticeae
and its relatives
Genes Genet. Syst. 73 (5), 297-309 (1998)
99185472
JOURNAL
MEDLINE
PUBMED
10085553
REFERENCE
2 (bases 1 to 604)
Sasanuma,T.
Direct Submission
Submitted (09-DEC-1998) Tsuneeo Sasanuma, Kyoto University,
Laboratory of Plant Genetics, Graduate School of Agriculture;
Sakyo-ku, Kitashirakawa Oiwakecho, Kyoto, Kyoto 606-8502, Japan
(E-mail:sasanuma@kais.kyoto-u.ac.jp, Tel:81-75-753-6145(ex.6145),
Fax:81-75-753-6146)
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BASE COUNT      122 a      184 c      169 g      129 t
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Query Match      59.5%; Score 192.2; DB 8; Length 604;
Best Local Similarity 80.1%; Pred. No. 3.3e-26;
Matches 238; Conservative 0; Mismatches 58; Indels 1; Gaps 1;
QY 2 GACCTCTGAAGCAGGTGGACTACCTGCTGCGCAACGGTGGATACCCCTGCTCGAGTTC 61
DB 306 GCCCTCTGAAGCAGGTGGACTACCTGCTGCGCAACGGTGGATACCCCTGCTCGAGTTC 365
QY 62 AGCAAGTTCGGCTTCGTGACCGGAGAACTCCACCTCCCGTGTACTACGACGGCCGC 121
DB 366 AGCAAGTTCGGCTTCGTGACCGGAGAACTCCACCTCCCGTGTACTACGACGGCCGC 425
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RESULT 14
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LOCUS
DEFINITION
Triticum urartu DNA for ribulose-1,5-bisphosphate
carboxylase/oxygenase small subunit, partial cds, clone Ura-B.
AB020954
ACCESSION
AB020954.1 GI:4038712
VERSION
Small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase.
Triticum urartu
SOURCE
Triticum urartu
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (sites)
Sasanuma,T. and Miyashita,N.T.
Subfamily divergence in the multigene family of
ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) in Triticeae
and its relatives
Genes Genet. Syst. 73 (5), 297-309 (1998)
99185472
JOURNAL
MEDLINE
PUBMED
10085553
REFERENCE
2 (bases 1 to 787)
Sasanuma,T.
Direct Submission
Submitted (09-DEC-1998) Tsuneeo Sasanuma, Kyoto University,
Laboratory of Plant Genetics, Graduate School of Agriculture;
Sakyo-ku, Kitashirakawa Oiwakecho, Kyoto, Kyoto 606-8502, Japan
(E-mail:sasanuma@kais.kyoto-u.ac.jp, Tel:81-75-753-6145(ex.6145),
Fax:81-75-753-6146)
FEATURES
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
4036.660 Million cell updates/sec

Title: US-09-987-899-5  
Perfect score: 323  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues 5105512  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	198.8	61.5	960	15	AAQ62173 rbcS subunit of ri
2	177	54.8	1110	24	ABK86728 Rice rubisco synth
3	125.6	38.9	471	24	ABL93405 Arabidopsis thalia
4	125.6	38.9	546	21	AAC48433 Arabidopsis thalia
5	125.6	38.9	572	21	AAC42417 Arabidopsis thalia
6	125.6	38.9	599	21	AAC47674 Arabidopsis thalia
7	125.6	38.9	681	24	ABQ65767 Arabidopsis thalia
8	125.6	38.9	724	24	ABL49453 Sequence #55 used

9	125.6	38.9	724	24	ABK30640 Plant dwarfing/stu
10	125.6	38.9	726	24	ABK30788 Plant dwarfing/stu
11	125.6	38.9	771	24	ABN99150 Arabidopsis thalia
12	125.6	38.9	785	24	ABN99094 Arabidopsis thalia
13	125.6	38.9	1164	21	AAC52133 Arabidopsis thalia
14	125.6	38.9	1205	24	ABN98273 Arabidopsis thalia
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18	124	38.4	739	24	ABK30768 Plant dwarfing/stu
19	123.2	38.1	570	21	AAK32041 Plant microsatelli
20	121.4	37.6	546	21	AAC48432 Arabidopsis thalia
21	121.4	37.6	632	24	ABQ66100 Arabidopsis thalia
22	121.4	37.6	767	24	ABN99163 Arabidopsis thalia
23	121.4	37.6	780	24	ABN99112 Arabidopsis thalia
24	121.4	37.6	1135	21	AAC51817 Arabidopsis thalia
25	117	36.2	606	21	AAK32043 Plant microsatelli
26	116.4	36.0	934	25	ABQ83212 Coffee rbcS protei
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28	107.8	33.4	2034	25	ABQ83211 Coffee rbcS gene S
29	107.2	33.2	453	24	ABL93846 Arabidopsis thalia
30	95.6	29.6	273	25	ABX30796 Human GDP-mannose
31	93	28.8	469	24	ABA92079 Arabidopsis RUBIS
32	92.2	28.5	502	21	AAK31309 Plant microsatelli
33	90.2	27.9	499	24	AAK35635 Nicotiana benthami
34	85.6	26.5	484	21	AAK31305 Plant microsatelli
35	84	26.0	479	21	AAK31292 Plant microsatelli
36	83	25.7	481	21	AAK31306 Plant microsatelli
37	79	24.5	479	21	AAK32042 Plant microsatelli
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39	74.2	23.0	477	21	AAC37237 Arabidopsis thalia
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44	60.6	18.8	336	16	AAQ87824 Agmenellum quadrup
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ALIGNMENTS

RESULT 1  
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ID AAQ62173 standard; cDNA; 960 BP.  
XX AAQ62173;  
AC AAQ62173;  
XX  
DT 16-NOV-1994 (first entry)  
XX  
DE rbcS subunit of ribulose-1,5-diphosphate carboxylase/oxidase.  
XX  
KW Ribulose-1,5-diphosphate carboxylase/oxidase; enzyme; rbcS;  
KW subunit; gene expression; induction; irradiation; light;  
KW promoter; plant; ss.  
XX  
OS Synthetic.  
XX  
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PN JP06070781-A.





PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0133456.  
PR 14-MAY-1999; 99US-0133418.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
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XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
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PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.

Query Match	38.9%;	Score 125.6;	DB 21;	Length 599;
Best Local Similarity	67.8%;	Pred. No. 2.5e-19;		
Matches 206;	Conservative	0;	Mismatches 94;	Indels 4; Gaps 2
Qy	1	CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGATACACCTGCTCGCTCGAGTT	60	
Db	290	CGAATTGGCTAAGGAAGTTGACTACCTTCTCCGCAACAAGTGGATTCCTTGTGTGTAATT	349	
Qy	61	C---AGCAAAGTCCGGTTCGTGTACCGCGAGAATCCACCTCCCGTGTACTACGACGG	117	
Db	350	CGAGTTAGACGACGGATTGTGTACCGTGCACGGAACAATCCCGGATACTACGATGG	409	
Qy	118	CCGCTACTCGACCATGTGGAAGCATGCCCATGTTCGGCTGCACGACGCCACCCAGGTGT	177	
Db	410	ACGGTACTCGACAATGTGGAAGC-TTCATTGTTCGGATGCACCGACTCCGCTCAAGTGT	468	
Qy	178	ACAAGAGCTGCAGGAGGCGCATCAATCCTACCCGGACGCTTCCACCGGTCATCGGCT	237	
Db	469	TGAAGGAAGTTGAAGAATGCAAGAGGAGTACCCCGGGCGCTTCATTAGATCATCGGAT	528	
Qy	238	TCGACAAACATCAAGCAGACGCGTAGTCGGTCAGCTTCATCGCTACAAGCCCCCGGGCAGCG	297	
Db	529	TCGACAAACCCCGTCAAGTCCGATGCATCAGTTTCATTTCGCTACAAGCCCCCAAGCTTCA	588	
Qy	298	ACTA	301	

589 CCGA 592

RESULT 7  
 ABQ65767/c  
 IIID ABQ65767 standard; DNA; 681 BP.  
 XX  
 XX AC ABQ65767;  
 DT 21-AUG-2002 (first entry)  
 XX DE Arabidopsis thaliana polynucleotide SEQ ID NO 344.  
 XX DE Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;  
 XX KW stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;  
 XX KW insecticide; antibiotic; da.  
 XX OS Arabidopsis thaliana.  
 XX PN US2002059663-Al.  
 XX PD 16-MAY-2002.  
 XX PF 26-JAN-2001; 2001US-0770149.  
 XX PR 27-JAN-2000; 2000US-178506P.  
 XX (GORL/) GORLACH J.  
 XX (ANY/) AN Y.  
 XX (HAML/) HAMILTON C M.  
 XX (PRIC/) PRICE J L.  
 XX (RAIN/) RAINES T M.  
 XX (YUYU/) YU Y.  
 XX (RAME/) RAMEAKA J G.  
 XX (PAGE/) PAGE A.  
 XX (MATH/) MATHAW A V.  
 XX (LEDF/) LEDFORD B L.  
 XX (WOES/) WOESSNER J P.  
 XX (HAAS/) HAAS W D.  
 XX (GARC/) GARCIA C A.  
 XX (KRIC/) KRICKER M.  
 XX (SLAT/) SLATER T.  
 XX (DAVI/) DAVIS K R.  
 XX (ALLE/) ALLEN K.  
 XX (HOFF/) HOFFMAN N.  
 XX (HURB/) HURBAN P.  
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
 XX Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
 XX Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
 XX Hurban P;  
 XX WPI; 2002-479224/51.  
 XX New nucleic acid that hybridizes to Arabidopsis thaliana sequences,  
 XX useful e.g. for preparing transgenic plants with increased resistance  
 XX or altered metabolism -  
 XX Claim 1; SEQ ID NO 344; 40pp + Sequence Listing; English.  
 XX The invention relates to nucleic acids (I) that hybridise under string-  
 XX conditions to any of 999 sequences (ABQ65424-ABQ66422) or their  
 XX fragments. (I) are used to express the corresponding polypeptides (II)  
 XX to produce genetically modified plant cells or transgenic plants, whi-  
 XX may have improved resistance to disease or stress, or altered  
 XX metabolic/biosynthetic pathways (for production of commercial,  
 XX nutritional or medicinal products), or generally any trait of interest  
 XX or can be used to screen for biologically active agents (e.g. fungicidal  
 XX insecticides and antibiotics).  
 XX Note: The sequence data for this patent did not form part of the prior  
 XX art specification, but was obtained in electronic format directly from the  
 XX USPTO at [seqdata.uspto.gov/sequence.html?docID=99909770149](http://seqdata.uspto.gov/sequence.html?docID=99909770149).

```
XX SQ Sequence 681 BP; 183 A; 143 C; 160 G; 195 T; 0 other;
Query Match 38.9%; Score 125.6; DB 24; Length 681;
Best Local Similarity 68.6%; Pred. No. 2.5e-18;
Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;

QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGTGGATACCTGCGCTCGAGTT 60
DB 472 CGAATTGGCTAAGGAAGTTCGACTACCTTCTCCGCAACAATGATTCCTTGTGTTGAATT 413

QY 61 C---AGCAAGTTCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGG 117
DB 412 CGAGTTGGACACCGGATTTGTGTACCGTGAGCAACGGAACACTCCCGGATACCTACGATGG 353

QY 118 CCGTACTGACCAATGTGGAAGCATGCCATGTTTCGGCTGCAACGACGCCACCCAGGTGT 177
DB 352 ACGGTACTGGACATGTGGAGGAGC-TTCCATGTTTCGGATGACCGATCCGCTCAAGTGT 294

QY 178 ACAAGGAGCTGCAGGAGCGCCATCAATCTTACCGGACGCTTCCACCGGTTCATCGGCT 237
DB 293 TGAAGGAAGTTGAAGATGCAAGAGGAGTACCGGCGGCTTCATTAGGATCATCGAT 234

QY 238 TCACACATCAAGACAGCAGCAGTGCCTGCTGCTTTCATCGCTTACAGCCCGCGGC 293
DB 233 TCACACACACCGCTCAAGTCCAAATGCATCAGTTTTCATTGCTTACAGCCCGCAAGC 178

RESULT 8
ABL49453
ID ABL49453 standard; cDNA; 724 BP.
XX AC ABL49453;
XX DT 01-JUL-2002 (first entry)
XX DE Sequence #55 used to create transgenic plant with dwarf phenotype.
XX KW Transgenic plant; dwarf phenotype; ss.
XX OS Arabidopsis thaliana.
XX PN WO200208411-A2.
XX PD 31-JAN-2002.
XX PF 20-JUL-2001; 2001WO-US23315.
XX PR 20-JUL-2000; 2000US-219943P.
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX PI Pogue GP, Della-Cioppa GR, Wolfe GM, Zheng W;
XX WPI; 2002-195875/25.
XX CC Creating transgenic plants exhibiting a dwarf phenotype useful in
PT pharmaceutical manufacturing, comprises expressing in the plant a
PT gene for dwarfism or stunting having a sequence selected from 122
PT polynucleotide sequences -
XX
XX Claim 1; Page 154; 178pp; English.
XX CC This invention relates to the creation of a transfect or transgenic
CC plant selected from ornamental, horticultural, forestry, medicinal and
CC Nicotiana sp. plants, all of which exhibit a dwarf phenotype by
CC expressing in the plant a DNA comprising a sequence selected from 122
CC polynucleotide sequences. This sequence represents on of those
CC polynucleotide sequences. The nucleic acid and amino acid sequences are
CC useful for producing transgenic plants exhibiting a dwarf phenotype for
CC use in pharmaceutical manufacturing. The cDNA sequences may be used
CC in recombinant DNA molecules to direct expression of polypeptides in
CC appropriate host cells.
```

XX	WPI; 2002-164823/21.	DT	23-APR-2002 (first entry)
XX		XX	Plant dwarfing/stunting related cDNA seq ID 202.
XX	Polynucleotide and amino acid sequences identified in one or more	XX	Plant; ss; dwarfism; stunting; EST; expressed sequence tag;
XX	metabolic pathways that lead to dwarfism and stunting in plants, useful	KW	transgenic plant; plant metabolism; contig.
PT	in agriculture to create dwarf varieties of any plant species -	XX	
XX		OS	Planta.
PS	Example 10; Fig 1; 717pp; English.	XX	
XX	The invention relates to polynucleotide and amino acid sequences	FN	WO200208410-A2.
CC	identified in one or more metabolic pathways that lead to dwarfism and	XX	
CC	stunting in plants. Also included are vectors comprising the	PD	31-JAN-2002.
CC	polynucleotides, transgenic plants (including the seed and leaf)	XX	
CC	transfected with the polynucleotides or vectors, a process for altering	PF	20-JUL-2001; 2001WO-US23120.
CC	the metabolism of a plant comprising providing the above vector and a	XX	
CC	plant, and transfecting the plant with the vector under conditions such	PR	20-JUL-2000; 2000US-219809P.
CC	that the metabolism of the plant is altered by expression of the isolated	PR	20-JUL-2000; 2000US-219810P.
CC	nucleic acid from the vector, e.g. such that a stunting phenotype in an	XX	
CC	industrial plant is produced and a process for the characterisation of	XX	(DOMC ) DOW CHEM CO.
CC	fractionated biological samples, comprising (a) providing one or more	PA	(REDD/) REDDY S A.
CC	apparatus, a mass spectroscopy apparatus or data analysis software and	PA	(LARR/) LARRINUA M I.
CC	(b) treating the fractionated biological samples and the reference	PA	(RUEG/) RUEGGER M.
CC	samples with the gas chromatography apparatus to generate chromatographic	PA	(WEG/) WEGLARZ T.
CC	data corresponding to the fractionated biological samples and the	PA	(BLAK/) BLAKESLEE B.
CC	reference samples, (c) treating the fractionated biological samples and	PA	(ORIE/) ORIEDO V B J.
CC	spectroscopic data corresponding to the fractionated biological samples	PA	(SAVI/) SAVICKAS J P.
CC	and the reference samples and (d) processing the chromatographic and the	PA	(MCCR/) MCCREY A D.
CC	spectroscopic data with the data analysis software. The nucleic acid and	PA	(MILL/) MILLER A B.
CC	the vector are useful for altering the metabolism of a plant and for	PA	(GACH/) GACHOTTE D.
CC	stunting a plant. The nucleic acids are useful in agriculture to create	PA	(GROS/) GROSLEY R.
CC	dwarf varieties of any plant species. The present sequence is a	PA	(PELL/) PELL R.
CC	plant EST, expressed sequence tag, isolated from a cDNA library and	XX	
CC	related to stunting/dwarfism.	XX	Reddy SA, Larrinua MT, Ruegger M, Weglarz T, Blakeslee B;
XX		PI	Oriedo VBJ, Savickas JP, McCrery AD, Miller AB, Pogue PG;
XX		PI	Della-Cioppa RG, Wolfe MG, Zheng W, Gachotte D, Grosley R, Pell R;
XX		XX	WPI; 2002-164823/21.
XX	Sequence 724 BP; 198 A; 174 C; 156 G; 196 T; 0 other;	DR	
XX		XX	
PT	Query Match 38.9%; Score 125.6; DB 24; Length 724;	PT	Polynucleotide and amino acid sequences identified in one or more
PT	Best Local Similarity 67.8%; Pred. No. 2.5e-18;	PT	metabolic pathways that lead to dwarfism and stunting in plants, useful
PT	Matches 206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;	PT	in agriculture to create dwarf varieties of any plant species -
XX		XX	Disclosure; Fig 4; 717pp; English.
QY	1 CGACCTCTGACGAGCTGACCTGCTGCGCAACGGCTGGATACCTCGCTCGAGTT 60	XX	
Db	279 CGAATTGGCTAAGGAAGTGTGCTACCTTCTCCGCAACAGTGGATTCCTGTGTGATT 338	XX	
QY	61 C---AGCAAGCTCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGGTGCTACTACGCG 117	XX	
Db	339 CGAGTTAGACACGGATTGTGTACCGTGAGCAGCGAAACACTCCCGGATACGATGG 398	XX	
QY	118 CCGTACTGGACCATGTGGAGCATGCCCATTGTTCCGCTGCAACGCGCACCAGGTGT 177	XX	
Db	399 ACGTACTGGACAATGTGGAAGC-TTCCATTGTTCCGATGACCGACTCCGCTCAAGTGT 457	XX	
QY	178 ACAGGAGCTCGAGGCGCATCAATCCTACCGGAGCCTTCCACCGGTGATCGGCT 237	XX	
Db	458 TGAAGGAAGTTGAAGATGCAAGAGGAGTACCCGGCGGCTTCATTAGATCATCGAT 517	XX	
QY	238 TCGAACATCAAGCAGCAGTGCCTGCTGCTTCATCGCTTCAACGCCCCCGGCGAGCG 297	XX	
Db	518 TCGACACACCGCTCAAGTCCATGATCATGTTTCATTGCTACAGCCCCCAAGCTTCA 577	XX	
QY	298 ACTA 301	XX	
Db	578 CCGA 581	XX	
XX		XX	
XX	RESULT 10	XX	
XX	ABK30788	XX	
XX	ID ABK30788 standard; cDNA; 726 BP.	XX	
XX	AC	XX	
XX	ABK30788;	XX	

XX	Sequence	726 BP; 194 A; 180 C; 156 G; 196 T; 0 other;	
XX	Query Match	38.9%; Score 125.6; DB 24; Length 726;	
XX	Best Local Similarity	67.8%; Pred. No. 2.5e-18;	
XX	Matches	206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;	
QY	1	CGACCTGCTGAAGCAGGTGACTACCTGTGCGCAACGGCTGATACCCCTGCGCTCGAGTT	60
DB	281	CGAATTGGCTAAGGAAGTTGACTACCTTCTCCGCAACAGTGGATTCTTTGTGTGAATT	340
QY	61	C---ACCAAGTGGCTTGTGTACCGCGAAGTCACTCCCTCCGTGCTACTACGACGG	117
DB	341	CGAGTTAGAGCACGGATTTGTGTACCGTGAACGCGAAGACACCTCCCGGATACCTACGATGG	400
QY	118	CCGCTACTGGACCATGTGGAAGCATGCCATGTTCCGCTGCAACGACGCCACCCAGGTGT	177
DB	401	ACGGTACTGGACAATGTGGAGC-TTCCATTGTTCGATGCACCGACTCCGCTCAAGTGT	459
QY	178	ACAAGGAGCTGCAGGAGGCCATCAAAATCCTTACCCGACGCTTCCACCGGTTCATCGGCT	237
DB	460	TGAAGGAAGTTGAAGATGCAAGAGGAGTACCCGGGGCTTTCATTAGATCATCGAT	519
QY	238	TCGACAACATCAAGCAGACGAGTGGCTGAGCTTCATTCGCTTCAAGCCCGGCGAGCG	297
DB	520	TCGACAACACCCGCTCAAGTCCAATGCATCAGTTTCATTGCTTCAAGCCCGGCGAGCTTCA	579
QY	298	ACTA 301	
DB	580	CCGA 583	
RESULT 11			
DE	ABN99150/C		
ID	ABN99150 standard; DNA; 771 BP.		
XX	AC	ABN99150;	
XX	DT	01-AUG-2002 (first entry)	
DE	Arabidopsis thaliana expressed polynucleotide SEQ ID NO 918.		
XX	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;		
KW	disease; crop; thale cress; tolerance factor; insect; pathogen;		
KW	nutrition; ds.		
OS	Arabidopsis thaliana.		
XX	US2002023281-A1.		
XX	21-FEB-2002.		
XX	26-JAN-2001; 2001US-0770445.		
XX	27-JAN-2000; 2000US-178472P.		
XX	(GORLACH J.		
PA	(ANYI/) AN Y.		
PA	(HAMI/) HAMILTON C M.		
PA	(PRIC/) PRICE J L.		
PA	(RAIN/) RAINES T M.		
PA	(YUY/) YU Y.		
PA	(RAME/) RAMEKA J G.		
PA	(PAGE/) PAGE A.		
PA	(MATH/) MATHW A V.		
PA	(LEDF/) LEDFORD B L.		
PA	(WOES/) WOESSNER J P.		
PA	(HAAS/) HAAS W D.		
PA	(GARC/) GARCIA C A.		
PA	(KRICK/) KRICKER M.		
PA	(SLAT/) SLATER T.		
PA	(DAVI/) DAVIS K R.		
PA	(ALLE/) ALLEN K.		
PA	(HOFF/) HOFFMAN N.		
PA	(HURE/) HURBAN P.		
PI	Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;		
PI	Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;		
PI	Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;		
PI	Hurban P;		
XX	WPI; 2002-400781/43.		
XX	New Arabidopsis thaliana nucleic acid for identifying homologous genes,		
PT	producing compositions that modulate the expression or function of its		
PT	encoded protein, and mapping functional regions of protein -		
XX	Claim 1; SEQ ID NO 918; 49pp + Sequence Listing; English.		
XX	The invention relates to an Arabidopsis thaliana nucleic acid (I)		
CC	comprising a sequence capable of hybridising under stringent conditions		
CC	to a sequence selected from any one of 999 sequences (ABN99231-		
CC	given in the specification or its fragment. A polypeptide (II) encoded by		
CC	(I), a transgenic plant (III) comprising an exogenous nucleic acid or a		
CC	genetically modified cell (IV) comprising an exogenous nucleic acid, is		
CC	useful for screening a candidate agent for its biological effect. (I) is		
CC	useful in identifying homologous or related genes, in producing		
CC	compositions that modulate the expression or function of its encoded		
CC	protein, mapping functional regions of the protein and in studying		
CC	associated physiological pathways. (I) is also useful for the genetic		
CC	manipulation of cells, particularly plant cells. (I) is also useful in		
CC	screening assays of various plant strains to determine the strains that		
CC	are best capable of withstanding a particular disease or environmental		
CC	stress. (II) and (III) are useful for screening of biologically active		
CC	agents, e.g. fungicides, insecticides, etc., for elucidating biochemical		
CC	pathways. The screened agents are useful in improved methods of treating		
CC	crops to prevent or treat disease. (II) are also useful in screening		
CC	programs to identify agents that mimic or enhance the action of tolerance		
CC	factors: Such agents are useful in improved methods of treating crops to		
CC	enhance their tolerance to environmental stress. (I) is also useful		
CC	for enhancing or inhibiting production of a biosynthetic product in a		
CC	plant. (III) is useful for identifying other mediators that may induce		
CC	expression of proteins of interest, for establishing the extent to which		
CC	any specific insect and/or pathogen is responsible for damage to a		
CC	particular plant, for identifying other mediators that enhance or induce		
CC	tolerance to environmental stress, for identifying factors involved in		
CC	biosynthetic pathways of nutritional, commercial, or medicinal value and		
CC	for identifying productions of nutritional, commercial or medicinal		
CC	value. (IV) is useful in the study of genetic function and regulation,		
CC	for alteration of the cellular metabolism and for screening compounds		
CC	that may affect the biological function of the gene or gene products.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from USPTO		
CC	at seqdata.uspto.gov/sequence.html?DocID=999909770445.		
XX	Sequence 771 BP; 215 A; 172 C; 185 G; 199 T; 0 other;		
XX	Query Match	38.9%; Score 125.6; DB 24; Length 771;	
XX	Best Local Similarity	67.8%; Pred. No. 2.5e-18;	
XX	Matches	206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;	
QY	1	CGACCTGCTGAAGCAGGTGACTACCTGTGCGCAACGGCTGATACCCCTGCGCTCGAGTT	60
DB	449	CGAATTGGCTAAGGAAGTTGACTACCTTCTCCGCAACAGTGGATTCTTTGTGTGAATT	390
QY	61	C---AGCAAGTTCGGCTTCGTGTACCGCGAGACTCCACTCCCTCCGTGCTACTACGACGG	117
DB	389	CGAGTTAGAGCACGGATTTGTGTACCGTGAACGCGAAGACACTCCCGGATACCTACGATGG	330
QY	118	CCGCTACTGGACCATGTGGAAGCATGCCATGTTCCGCTGCAACGACGCCACCCAGGTGT	177
DB	329	ACGGTACTGGACAATGTGGAGC-TTCCATTGTTCGATGCACCGACTCCGCTCAAGTGT	271
QY	178	ACAAGGAGCTGCAGGAGGCCATCAATCCTACCCGACGCTTCCACCGGCTCATCGGCT	237
DB	270	TGAAGGAAGTTGAAGAATGCAAGAGGAGTACCCGGGGCTTTCATTAGGATCATCGAT	211

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QY 238 TCGACACATCAGACGACGCGTTCAGCTTCATCGCTACAGCCCCCGGCGACG 297
DB 210 TCGACACACCCGCTCAAGTCCATGTCATGATTCATTCGCTACAGCCCCCAAGTTCA 151
QY 298 ACTA 301
DB 150 CCGA 147

RESULT 12
ID ABN99094/c
XX ABN99094 standard; DNA; 785 BP.
AC ABN99094;
XX
DT 01-AUG-2002 (first entry)
XX
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 862.
XX
KW Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
KW disease; crop; thale cress; tolerance factor; insect; pathogen;
KW nutrition; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2002023281-A1.
XX
PD 21-FEB-2002.
XX
XX 26-JAN-2001; 2001US-0770445.
XX
PR 27-JAN-2000; 2000US-178472P.
XX
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J C.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDE/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
WPI; 2002-400781/43.
XX
XX
PT New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein -
XX
XX
PS Claim 1; SEQ ID NO 862; 49pp + Sequence Listing; English.
XX
XX
CC The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridising under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
```

```
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful
CC for enhancing or inhibiting production of a biosynthetic product in a
CC plant. (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocId=999909770445.
XX
SQ Sequence 785 BP; 226 A; 155 C; 193 G; 211 T; 0 other;
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Query Match 38.9%; Score 125.6; DB 24; Length 785;

Best Local Similarity 68.6%; Pred. No. 2.5e-18; Indels 4; Gaps 2;

Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;

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QY 61 C---AGCAAGGTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGCTGCTACTACGCG 117
DB 471 CGAGTTGGAGCAGCGGATTTGTGTACCGTGAGCACGGTAACCTACCCGGATATGATGG 412
QY 118 CGGCTACTGAGCATGTGGAAGCATCCCATGTTCCGCTTGCAACGACGCCACCGAGTGT 177
DB 411 ACGTACTGACAAATGTGAAGG-TTCCCTTGTTCGGTTGACCCGACTCGCTCAAGTGT 353
QY 178 ACAAGGAGCTGCAGGAGGCCATCAATCTACCCGGACGCGCTTCCACCGGTCATCGGCT 237
DB 352 TGAAGGAAGTGGAGAGAGTGCAGAGAGGTACCCCAATGCCTTCATTAGGATCATCGAT 293
QY 238 TCGACAAACATCAAGCAGACGCGTGCAGCTTCATCGCTACAGCCCCCGGCG 293
DB 292 TCGACAAACCCCGTCAAGTCCAGTGCATGATTCATTCGCTTCAAGCCACCAAGC 237
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RESULT 13

AAC52133

ID AAC52133 standard; DNA; 1164 BP.

XX

AC AAC52133;

XX 18-OCT-2000 (first entry)

DT

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70444.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN	EF1033405-A2.	PR	01-JUL-1999;	99US-0142154.
XX		PR	02-JUL-1999;	99US-0142055.
PD	06-SEP-2000.	PR	06-JUL-1999;	99US-0142390.
XX		PR	08-JUL-1999;	99US-0142803.
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XX	25-FEB-2000; 2000EP-0301439.	PR	12-JUL-1999;	99US-0142977.
PR		PR	13-JUL-1999;	99US-0143542.
PR		PR	14-JUL-1999;	99US-0143624.
PR		PR	15-JUL-1999;	99US-0144005.
PR		PR	16-JUL-1999;	99US-0144085.
PR		PR	16-JUL-1999;	99US-0144086.
PR		PR	19-JUL-1999;	99US-0144325.
PR		PR	19-JUL-1999;	99US-0144331.
PR		PR	19-JUL-1999;	99US-0144332.
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PR		PR	20-JUL-1999;	99US-0144684.
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PR		PR	27-JUL-1999;	99US-0145919.
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PR		PR	27-AUG-1999;	99US-0151080.
PR		PR	30-AUG-1999;	99US-0151303.
PR		PR	31-AUG-1999;	99US-0151438.
PR		PR	01-SEP-1999;	99US-0151930.
PR		PR	07-SEP-1999;	99US-0152363.
PR		PR	10-SEP-1999;	99US-0153070.
PR		PR	13-SEP-1999;	99US-0153758.
PR		PR	15-SEP-1999;	99US-0154018.
PR		PR	16-SEP-1999;	99US-0154039.

PR	20-SEP-1999;	99US-0154779.	XX	XX	Arabidopsis thaliana expressed polynucleotide SEQ ID NO 41.
PR	22-SEP-1999;	99US-0155139.	XX	XX	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
PR	23-SEP-1999;	99US-0155486.	KW	KW	disease; crop; thale cress; tolerance factor; insect; pathogen;
PR	24-SEP-1999;	99US-0155659.	KW	KW	nutrition; ds.
PR	28-SEP-1999;	99US-0156458.	OS	OS	Arabidopsis thaliana.
PR	29-SEP-1999;	99US-0156596.	XX	XX	US2002023281-A1.
PR	04-OCT-1999;	99US-0157117.	XX	XX	21-FEB-2002.
PR	05-OCT-1999;	99US-0157753.	PD	PD	26-JAN-2001; 2001US-0770445.
PR	06-OCT-1999;	99US-0157865.	XX	XX	27-JAN-2000; 2000US-178472P.
PR	07-OCT-1999;	99US-0158029.	PF	PF	(GORL/) GORLACH J.
PR	08-OCT-1999;	99US-0158232.	XX	XX	(ANY/) AN Y.
PR	12-OCT-1999;	99US-0158369.	PA	PA	(HAMI/) HAMILTON C M.
PR	13-OCT-1999;	99US-0159293.	PA	PA	(PRIC/) PRICE J L.
PR	13-OCT-1999;	99US-0159295.	PA	PA	(RAIN/) RAINES T M.
PR	14-OCT-1999;	99US-0159329.	PA	PA	(YUY/) YU Y.
PR	14-OCT-1999;	99US-0159330.	PA	PA	(RAME/) RAMEAKA J G.
PR	14-OCT-1999;	99US-0159331.	PA	PA	(PAGE/) PAGE A.
PR	14-OCT-1999;	99US-0159637.	PA	PA	(MATH/) MATHAW A V.
PR	14-OCT-1999;	99US-0159638.	PA	PA	(LEDF/) LEDFORD B L.
PR	18-OCT-1999;	99US-0159584.	PA	PA	(WOES/) WOESSNER J P.
PR	21-OCT-1999;	99US-0160741.	PA	PA	(HAAS/) HAAS W D.
PR	21-OCT-1999;	99US-0160768.	PA	PA	(GARC/) GARCIA C A.
PR	21-OCT-1999;	99US-0160770.	PA	PA	(KRIC/) KRICKER M.
PR	21-OCT-1999;	99US-0160814.	PA	PA	(SLAT/) SLATER T.
PR	21-OCT-1999;	99US-0160815.	PA	PA	(DAVI/) DAVIS K R.
PR	22-OCT-1999;	99US-0160980.	PA	PA	(ALLE/) ALLEN K.
PR	22-OCT-1999;	99US-0160981.	PA	PA	(HOFF/) HOFFMAN N.
PR	22-OCT-1999;	99US-0160989.	PA	PA	(HURB/) HURBAN P.
PR	25-OCT-1999;	99US-0161404.	XX	XX	Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PR	25-OCT-1999;	99US-0161405.	PI	PI	Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PR	25-OCT-1999;	99US-0161406.	PI	PI	Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PR	26-OCT-1999;	99US-0161359.	PI	PI	Hurban P;
PR	26-OCT-1999;	99US-0161360.	XX	XX	WPI; 2002-400781/43.
PR	26-OCT-1999;	99US-0161361.	DR	DR	New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PR	28-OCT-1999;	99US-0161920.	PT	PT	producing compositions that modulate the expression or function of its
PR	28-OCT-1999;	99US-0161922.	PT	PT	encoded protein, and mapping functional regions of protein
PR	28-OCT-1999;	99US-0161993.	XX	XX	Claim 1; SEQ ID NO 41; 49pp + Sequence Listing; English.
PR	29-OCT-1999;	99US-0162142.	PS	PS	The invention relates to an Arabidopsis thaliana nucleic acid (I)
QY	1	CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGATT	CC	CC	comprising a sequence capable of hybridizing under stringent conditions
Db	676	CGAATTGGCTAAGGAAGTTGACTACTTATCCGCAACAAGTGGATTCTTGTGTGAATT	CC	CC	to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
QY	61	C---AGCAGGTGCGCTTCGTGTACCGGAGAACTCCACCTCCCGGTGCTACTACGACGG	CC	CC	given in the specification or its fragment. A polypeptide (II) encoded by
Db	736	CGAGTTGGAGCAGCGAATTGTGTACCGTGAGCAGCGTAATCACC CGGATACTATGATGG	CC	CC	(I), a transgenic plant (III) comprising an exogenous nucleic acid or a
QY	118	CCGCTACTGGACCATGTGGAAGCATGCCCATGTTTCGGCTGCAACGACGCCACCCAGGTGT	CC	CC	genetically modified cell (IV) comprising an exogenous nucleic acid, is
Db	796	ACGTTACTGGACATGTGGAAGC-ITCCCTTGTTCGGTTGACCGACTCCGCTCAAGTGT	CC	CC	useful for screening a candidate agent for its biological effect. (I) is
QY	178	ACAAGGAGCTGCAGAGGCCATCAATCCTTACCGGAGCGCTTCACCGGTCAATCGGCT	CC	CC	useful in identifying homologous or related genes, in producing
Db	855	TGAAGGAAGTGAAGAGTGAAGAGAGTACCCCAATGCCCTTATTAGGATCATCGGAT	CC	CC	compositions that modulate the expression or function of its encoded
QY	238	TGCACACATCAGCAGACGAGTCGTCAGCTTCATCGCTTACAGCCCGCCGCGC	CC	CC	protein, mapping functional regions of the protein and in studying
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	associated physiological pathways. (I) is also useful for the genetic
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	manipulation of cells, particularly plant cells. (I) is also useful in
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	screening assays of various plant strains to determine the strains that
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	are best capable of withstanding a particular disease or environmental
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	stress. (II) and (III) are useful for screening of biologically active
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	pathways. The screened agents are useful in improved methods of treating
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	crops to prevent or treat disease. (II) are also useful in screening
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	programs to identify agents that mimic or enhance the action of tolerance
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	factors. Such agents are useful in improved methods of treating crops to
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	enhance their tolerance to environmental stress. (I) is also useful
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	for enhancing or inhibiting production of a biosynthetic product in a
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	plant. (III) is useful for identifying other mediators that may induce
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
Db	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
QY	915	TCGACACACCCGTCAGTCAGTCCAGTTCAGTTTCATTTGCTTACAGCCACCAAGC	CC	CC	
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 17:13:01 ; Search time 1942 Seconds  
(without alignments)  
4042.403 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
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- 22: em\_gss\_nam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	311	96.3	466	12	BI273504	BI273504 949026D10
3	311	96.3	471	12	BI245249	BI245249 949026D10
4	311	96.3	489	10	BG549370	BG549370 947074H12

5	311	96.3	566	12	BI478737	BI478737 949068G08
6	311	96.3	578	12	BI396085	BI396085 949044B04
7	311	96.3	580	12	BI674933	BI674933 949076E10
8	311	96.3	588	12	BG842079	BG842079 MEST35-H0
9	311	96.3	589	12	BI319097	BI319097 949039C04
10	311	96.3	619	12	BI430981	BI430981 949063F09
11	311	96.3	622	10	BG458523	BG458523 947045B08
12	311	96.3	652	9	AM352495	AM352495 707050B11
13	310	96.0	817	9	AA979879	AA979879 MEST3-G2
14	309.4	95.8	475	12	BI319103	BI319103 949039D04
15	309.4	95.8	553	10	BE055905	BE055905 945017B11
16	309.4	95.8	629	9	AW331243	AW331243 707050B11
17	307.8	95.3	1172	11	AY103730	AY103730 Zea mays
18	307.4	95.2	831	10	BG319747	BG319747 Zm03_05H0
19	307	95.0	574	10	BG517358	BG517358 947061E01
20	306.2	94.8	915	12	BG837761	BG837761 Zm10_05H0
21	306	94.7	495	12	BI643447	BI643447 949076E10
22	304.6	94.3	665	12	BM266503	BM266503 MEST382-B
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24	295.2	91.4	704	10	BG320087	BG320087 Zm03_01G0
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27	289	89.5	513	12	BI431142	BI431142 949059C09
28	287	88.9	471	10	BG550428	BG550428 947074H12
29	287	88.9	521	12	BI595975	BI595975 949075C03
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31	276.2	85.5	673	12	BM078545	BM078545 MEST121-B
32	272.6	84.4	489	10	BG458372	BG458372 947044G04
33	271	83.9	638	12	BI993279	BI993279 1020075F0
34	271	83.9	655	12	BG842727	BG842727 MEST39-D0
35	271	83.9	732	12	BM080707	BM080707 MEST112-C
36	271	83.9	745	12	BG842572	BG842572 MEST33-E0
37	269.4	83.4	493	10	BE924836	BE924836 947011G10
38	268.8	83.2	550	12	BI674604	BI674604 949022F06
39	268.6	83.2	565	12	BI644173	BI644173 949022F06
40	267.2	82.7	445	12	BI675118	BI675118 949077G05
41	265.6	82.2	558	12	BI643515	BI643515 949077G05
42	265.6	82.2	570	12	BI675117	BI675117 949077G05
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ALIGNMENTS

RESULT 1  
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DEFINITION 949026D10.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose  
Ze mays cDNA, mRNA sequence.  
ACCESSION BI319160  
VERSION BI319160.1 GI:14997085  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 343)  
AUTHORS Walbot V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
JOURNAL Unpublished  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949026 row: D column: 10.  
Location/Qualifiers

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/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site: 1: EcoRI; Site: 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal shoots 3 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."
BASE COUNT      70 a 126 c 94 g 53 t
ORIGIN
Query Match      96.3%; Score 311; DB 12; Length 343;
Best Local Similarity 99.7%; Pred. No. 2.7e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGGCGACGGCTGGATACCTGCTCGAGTT 60
Db 6 CGACCTGCTGAAGCAGGTGAGTACCTGCTGGCGACGGCTGGATACCTGCTCGAGTT 65
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Db 245 ACAACATCAAGCAGACGAGTGGTGTGAGCTTTCATCGCTTACAGCCCGCGGAGGACT 304
QY 301 AGACCGCGCGCGCGCGCGCGCC 323
Db 305 AGACCGCGCGCGCGCGCGCGCC 327

RESULT 2
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LOCUS      949026D10.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION BI273504
VERSION    BI273504.1 GI:14883710
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 466)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University

Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949026 row: D column: 10.
Location/Qualifiers
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/db_xref="taxon:4577"
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/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site: 1: EcoRI; Site: 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal shoots 3 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."
BASE COUNT      88 a 130 c 163 g 85 t
ORIGIN
Query Match      96.3%; Score 311; DB 12; Length 466;
Best Local Similarity 99.7%; Pred. No. 2.8e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGGCGACGGCTGGATACCTGCTCGAGTT 60
Db 426 CGACCTGCTGAAGCAGGTGAGTACCTGCTGGCGACGGCTGGATACCTGCTCGAGTT 367
QY 61 CAGCAGGTGGCTTGGTGACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 120
Db 366 CAGCAGGTGGCTTGGTGACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 307
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Db 306 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 248
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Db 247 AGAGCTGAGGAGGCCATCAATCTTACCGGAGCGCTTCCACCGCTCATCGGCTTCG 188
QY 241 ACAACATCAAGCAGACGAGTGGTGTGAGCTTTCATCGCTTACAGCCCGCGGAGGACT 300
Db 187 ACAACATCAAGCAGACGAGTGGTGTGAGCTTTCATCGCTTACAGCCCGCGGAGGACT 128
QY 301 AGACCGCGCGCGCGCGCGCGCC 323
Db 127 AGACCGCGCGCGCGCGCGCGCC 105

RESULT 3
BI245249/c
LOCUS      949026D10.x1 949 - Juvenile leaf and shoot cDNA from Steve Moose
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION BI245249
VERSION    BI245249.1 GI:14717599
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KEYWORDS EST.
SOURCE Zea mays
ORGANISM

REFERENCE 1 (bases 1 to 471)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished
          Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 949026 row: D column: 10.

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                /lab_host="E. coli XL0LR"
                /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
                /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 88 a 133 c 164 g 86 t
ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 471;
Best Local Similarity 99.7%; Pred. No. 2.8e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 60
DB 426 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 367

QY 61 CAGCAAGTTCGGCTTCGCTGACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
DB 366 CAGCAAGTTCGGCTTCGCTGACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 307

QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 180
DB 306 CTACTGGACCATGTGGAAGC-TGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 248

QY 181 AGAGCTGAGAGGCGCATCAATCTACCGGACGCGCTTCACCGCGTCACTCGGTTTCG 240
DB 247 AGAGCTGAGAGGCGCATCAATCTACCGGACGCGCTTCACCGCGTCACTCGGTTTCG 188

QY 241 ACAACATCAAGCAGCGAGTGGTTCAGTTCATCGCCTACAGCCCCCGGCGAGGACT 300
DB 187 ACAACATCAAGCAGCGAGTGGTTCAGTTCATCGCCTACAGCCCCCGGCGAGGACT 128

QY 301 AGACCGCGCCCGCGCGCCCC 323
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DB 127 AGACCGCGCCCGCGCGCCCC 105

RESULT 4
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LOCUS 489 bp mRNA linear EST 05-APR-2001
DEFINITION 947074H12.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA sequence.
ACCESSION BG549370
VERSION BG549370.1 GI:13558014
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 489)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished
          Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
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BASE COUNT 92 a 179 c 135 g 83 t
ORIGIN

Query Match 96.3%; Score 311; DB 10; Length 489;
Best Local Similarity 99.7%; Pred. No. 2.9e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 60
DB 136 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 195

QY 61 CAGCAAGTTCGGCTTCGCTGACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
DB 196 CAGCAAGTTCGGCTTCGCTGACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 255

QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 180
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QY 241 ACAACATCAAGCAGCGAGTGGTTCAGTTCATCGCCTACAGCCCCCGGCGAGGACT 300
DB 375 ACAACATCAAGCAGCGAGTGGTTCAGTTCATCGCCTACAGCCCCCGGCGAGGACT 434

QY 301 AGACCGCGCCCGCGCGCCCC 323
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Db 435 AGACCGCGCCCGCGCGCCGCC 457
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BI478737 566 bp mRNA linear EST 27-AUG-2001
949068G08.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
Zea mays cDNA, mRNA sequence.
BI478737
ACCESSION BI478737.1 GI:15313513
VERSION 1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Walbot.V.
AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE University
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Moose"
/notes="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybridzap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
BASE COUNT 107 a 205 c 162 g 92 t
ORIGIN
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Best Local Similarity 99.7%; Pred. No. 3e-61;
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Db 200 CGACCTGCTGAACGAGTGGAGTACTGCTGGCGAACGCTGATACCTGCTCGAGTT 259
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QY 61 CAGCAGAGTTCGGTTCGCTGACCGGAGAACTCCACCTCCCGTGTACTACGACGCCG 120
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RESULT 5
BI478737
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DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION BI396085
VERSION BI396085.1 GI:15100294
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Walbot.V.
AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE University
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949044 row: B column: 04.
Location/Qualifiers
1..578
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"
/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative
meristem"
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
/notes="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybridzap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
BASE COUNT 106 a 214 c 163 g 95 t
ORIGIN
Query Match 96.3%; Score 311; DB 12; Length 578;
Best Local Similarity 99.7%; Pred. No. 3e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGACCTGCTGAACGAGTGGAGTACTGCTGGCGAACGCTGATACCTGCTCGAGTT 60
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Db 191 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 250
QY 61 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
Db 251 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 310
QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180
Db 311 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 369
QY 181 AGGAGCTGCAGAGGGCCATCAATCTACCCGAGCGCTTCCACCGCTCATCGGTTGCG 240
Db 370 AGGAGCTGCAGAGGGCCATCAATCTACCCGAGCGCTTCCACCGCTCATCGGTTGCG 429
QY 241 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 300
Db 430 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 489
QY 301 AGACCGCGCCCGCGCGCCCGCC 323
Db 490 AGACCGCGCCCGCGCGCCCGCC 512

RESULT 7
Bi674933
LOCUS
DEFINITION
Zea mays cDNA, mRNA sequence.
ACCESSION
Bi674933
VERSION
Bi674933.1 GI:15590317
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 580)
Walbot.V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949076 row: E column: 10.
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"
/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative
meristem"
/seq_id="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
/note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybridz vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
```

```
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
BASE COUNT 108 a 215 c 168 g 89 t
ORIGIN
Query Match 96.3%; Score 311; DB 12; Length 580;
Best Local Similarity 99.7%; Pred. No. 3e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 60
Db 226 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 285
QY 61 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
Db 286 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 345
QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180
Db 346 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 404
QY 181 AGGAGCTGCAGAGGGCCATCAATCTACCCGAGCGCTTCCACCGCTCATCGGTTGCG 240
Db 405 AGGAGCTGCAGAGGGCCATCAATCTACCCGAGCGCTTCCACCGCTCATCGGTTGCG 464
QY 241 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 300
Db 465 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 524
QY 301 AGACCGCGCCCGCGCGCCCGCC 323
Db 525 AGACCGCGCCCGCGCGCCCGCC 547

RESULT 8
Bi674933
LOCUS
DEFINITION
MEST35-H09.T3 ISUM3-TL Zea mays cDNA clone MEST35-H09 3', mRNA
sequence.
ACCESSION
Bi674933
VERSION
Bi674933.1 GI:14208401
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 588)
Qiu.F., Cui.F., Guo.L., Ashlock,D.A, Wen.T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG) .
Location/Qualifiers
1..588
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST35-H09"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/clone_lib="ISUM3-TL"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
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ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAAGATTGCGCCGCGAGGAATTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector."

BASE COUNT	149 a	143 c	168 g	108 t
ORIGIN				
Query Match	96.3%; Score 311; DB 12; Length 588;			
Best Local Similarity	99.7%; Pred. No. 3e-61;			
Matches 322; Conservative	0; Mismatches 0; Indels 1; Gaps 1;			
QY	1 CGACCTGCTGACGAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 120			
Db	577 CGACCTGCTGACGAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 518			
QY	61 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 120			
Db	517 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 458			
QY	121 CTACTGGACATGTGAAGATGCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180			
Db	457 CTACTGGACATGTGAAGG-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 399			
QY	181 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 240			
Db	398 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 339			
QY	241 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 300			
Db	338 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 279			
QY	301 AGACCGCGCGCGCGCGCGCGCC 323			
Db	278 AGACCGCGCGCGCGCGCGCGCC 256			

RESULT 9  
BI319097/c  
LOCUS 949039C04.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose  
DEFINITION Zea mays cDNA, mRNA sequence.  
ACCESSION BI319097  
VERSION BI319097.1 GI:14996976  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 589)  
Walbot,V.  
Maize ESTs from various cDNA libraries sequenced at Stanford University  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949039 row: C column: 04.  
Location/Qualifiers  
1..589  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W64A"

ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dt primer (5' AACTGGAAGATTGCGCCGCGAGGAATTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector."

BASE COUNT 149 a 143 c 168 g 108 t

ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 588;

Best Local Similarity 99.7%; Pred. No. 3e-61;

Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGACGAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 60

Db 577 CGACCTGCTGACGAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 518

QY 61 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 120

Db 517 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 458

QY 121 CTACTGGACATGTGAAGATGCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180

Db 457 CTACTGGACATGTGAAGG-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 399

QY 181 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 240

Db 398 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 339

QY 241 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 300

Db 338 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 279

QY 301 AGACCGCGCGCGCGCGCGCGCC 323

Db 278 AGACCGCGCGCGCGCGCGCGCC 256

RESULT 9

BI319097/c

LOCUS 949039C04.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose

DEFINITION Zea mays cDNA, mRNA sequence.

ACCESSION BI319097

VERSION BI319097.1 GI:14996976

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 589)

Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 949039 row: C column: 04.

Location/Qualifiers

1..589

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W64A"

/db xref="taxon:4577"

/tissue type="immature leaf primordium and vegetative meristem"

/dev stage="4 stages from 3-13 days after imbibing"

/lab\_host="E. coli XL0LR"

/clone lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"

/notes="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 141 a 155 c 197 g 96 t

ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 589;

Best Local Similarity 99.7%; Pred. No. 3e-61; 0; Indels 1; Gaps 1;

Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGAAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 60

Db 502 CGACCTGCTGAAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 443

QY 61 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 120

Db 442 CAGCAAGGTGCGGCTTCTGCTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCGG 383

QY 121 CTACTGGACATGTGAAGATGCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180

Db 382 CTACTGGACATGTGAAGG-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 324

QY 181 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 240

Db 323 AGGAGCTGAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCTACGCGGCTTCG 264

QY 241 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 300

Db 263 ACAACATCAAGCAGACGAGTGGCTCAGCTTTCATCGCCTTCAAGCCCCCGGCGAGGACT 204

QY 301 AGACCGCGCGCGCGCGCGCGCC 323

Db 203 AGACCGCGCGCGCGCGCGCGCC 181

RESULT 10

BI430981

LOCUS 949063P09.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose

DEFINITION Zea mays cDNA, mRNA sequence.

ACCESSION BI430981

VERSION BI430981.1 GI:15209097

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 619)

Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Contact: Walbot V

Department of Biological Sciences

Stanford University



855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949063 row: F column: 09.

FEATURES source

Location/Qualifiers  
1. .619  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W64A"  
/db\_xref="taxon:4577"  
/tissue\_type="immature leaf primordium and vegetative meristem"  
/dev\_stage="4 stages from 3-13 days after imbibing"  
/lab\_host="E. coli XL0LR"  
/clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"  
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site\_1: EcoRI; Site\_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 110 a 225 c 177 g 107 t  
ORIGIN  
Query Match 96.3%; Score 311; DB 12; Length 619;  
Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1;  
Matches 322; Conservative 0; Mismatches 0;

QY 1 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 60  
DB 208 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 267  
QY 61 CAGCAGGTGCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 120  
DB 268 CAGCAGGTGCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 327  
QY 121 CTACTGGACCATGTGGAAGC-TGCCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACA 180  
DB 328 CTACTGGACCATGTGGAAGC-TGCCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACA 386  
QY 181 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240  
DB 387 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 446  
QY 241 ACAACATCAAGCAGACGAGTGGCTGAGTTTCATCGCTTACAAGCCCCGGGACGAGT 300  
DB 447 ACAACATCAAGCAGACGAGTGGCTGAGTTTCATCGCTTACAAGCCCCGGGACGAGT 506  
QY 301 AGACCGCGCCCGCGCGCCCC 323  
DB 507 AGACCGCGCCCGCGCGCCCC 529

RESULT 11  
BG458523  
LOCUS 947045808.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA  
DEFINITION BG458523 622 bp mRNA linear EST 19-MAR-2001  
sequence.  
ACCESSION BG458523  
VERSION BG458523.1 GI:13381848  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 622)  
Walbot V.  
Maize ESTs from various cDNA libraries sequenced at Stanford University  
Unpublished  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave., Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 947045 row: B column: 08.

FEATURES source

Location/Qualifiers  
1. .622  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf and stem, including leaf base"  
/dev\_stage="2 week old seedling (3 leaves)"  
/lab\_host="XLI-Blue"  
/clone\_lib="947 - 2 week shoot from Barkan lab"  
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-); Site 1: EcoRI; Site 2: XhoI; Directionally cloned using Stratagene's Unizap\_XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10<sup>5</sup> independent recombinant phage. The plants were greenhouse grown."

BASE COUNT 117 a 224 c 172 g 109 t  
ORIGIN  
Query Match 96.3%; Score 311; DB 10; Length 622;  
Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1;  
Matches 322; Conservative 0; Mismatches 0;

QY 1 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 60  
DB 244 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 303  
QY 61 CAGCAAGTTCGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTACTACGACGGCG 120  
DB 304 CAGCAAGTTCGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTACTACGACGGCG 363  
QY 121 CTACTGGACCATGTGGAAGCATGCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACA 180  
DB 364 CTACTGGACCATGTGGAAGC-TGCCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACA 422  
QY 181 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240  
DB 423 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 482  
QY 241 ACAACATCAAGCAGACGAGTGGCTGAGTTTCATCGCTTACAAGCCCCGGGACGAGT 300  
DB 483 ACAACATCAAGCAGACGAGTGGCTGAGTTTCATCGCTTACAAGCCCCGGGACGAGT 542  
QY 301 AGACCGCGCCCGCGCGCCCC 323  
DB 543 AGACCGCGCCCGCGCGCCCC 565

RESULT 12  
AW352495  
LOCUS 707050B11.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea  
DEFINITION AW352495 652 bp mRNA linear EST 02-FEB-2000  
mays cDNA, mRNA sequence.  
ACCESSION AW352495  
VERSION AW352495.1 GI:6851485  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE AUTHORS TITLE JOURNAL COMMENT	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
	1 (bases 1 to 652)	
	Walbot.V.	
	Maize ESTs from various cDNA libraries sequenced at Stanford University	
JOURNAL COMMENT	Unpublished	
	Contact: Walbot V	
	Department of Biological Sciences	
	Stanford University	
JOURNAL COMMENT	855 California Ave, Palo Alto, CA 94304, USA	
	Tel: 650 723 2227	
	Fax: 650 725 8221	
	Email: walbot@stanford.edu	
JOURNAL COMMENT	Plate: 707050 row: B column: 11.	
	Location/Qualifiers	
	1..652	
	/organism="Zea mays"	
JOURNAL COMMENT	/mol_type="mRNA"	
	/cultivar="W23"	
	/db_xref="taxon:4577"	
	/tissue_type="tassel, kernel, silk, husk, root, leaf"	
JOURNAL COMMENT	/dev_stage="adult"	
	/lab_host="DH10B"	
	/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"	
	)	
JOURNAL COMMENT	/notes="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."	
	BASE COUNT 130 a 237 c 185 g 100 t	
	ORIGIN	
JOURNAL COMMENT	Query Match 96.3%; Score 311; DB 9; Length 652;	
	Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1;	
	Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
	QY 1 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 60	
JOURNAL COMMENT	Db 286 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 345	
	QY 61 CAGCAAGGTGGCTTGTGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 120	
	Db 346 CAGCAAGGTGGCTTGTGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 405	
	QY 121 CTACTGGACCATGTGGAGCATGCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180	
JOURNAL COMMENT	Db 406 CTACTGGACCATGTGGAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 464	
	QY 181 AGGAGCTGCGAGGAGCCATCAATCTCTACCGGACGCTTCCACCGGTCTCG 240	
	Db 465 AGGAGCTGCGAGGAGCCATCAATCTCTACCGGACGCTTCCACCGGTCTCG 524	
	QY 241 ACAACATCAAGCAGACGAGTGGTCACTTCATCGCTACAAGCCCCGGGAGGACT 300	
JOURNAL COMMENT	Db 525 ACAACATCAAGCAGACGAGTGGTCACTTCATCGCTACAAGCCCCGGGAGGACT 584	
	QY 301 AGACCGCGCCCGCGCGCGCC 323	
	Db 585 AGACCGCGCCCGCGCGCGCC 607	
JOURNAL COMMENT	RESULT 13	
	AA979879	
	LOCUS	
	DEFINITION AA979879 817 bp mRNA linear EST 26-MAY-1998	
JOURNAL COMMENT	MEST2-G2.TW1412.Seq ISUM2 Zea mays cDNA clone MEST2-G2 5', mRNA	
	sequence.	
	AA979879	
	VERSION AA979879.1 GI:3157257	
JOURNAL COMMENT	KEYWORDS EST.	
	Zea mays	
	SOURCE	
	Zea mays	
JOURNAL COMMENT	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
	1 (bases 1 to 817)	
	Wen,T.J., Ashlock,D.A. and Schnable,P.S.	
	Expressed Sequence Tags from B73 Maize Seedlings	
JOURNAL COMMENT	Unpublished	
	Contact: Schnable, PS	
	Schnable Laboratory	
	Iowa State University	
JOURNAL COMMENT	G405 Agronomy, Ames, IA 50011, USA	
	Tel: (515)-294-0975	
	Fax: (515)-294-2299	
	Email: schnable@iastate.edu	
JOURNAL COMMENT	PCR Primers	
	FORWARD: tw1412 (5'-GAAGATACCCCAACCAACC-3')	
	BACKWARD: T7-YJ (5'-TAATACGACTCATATAGGC-3')	
	Plate: MEST2 row: G column: 2	
JOURNAL COMMENT	Seq primer: tw1412 (5'-GAAGATACCCCAACCAACC-3').	
	Location/Qualifiers	
	1..817	
	/organism="Zea mays"	
JOURNAL COMMENT	/mol_type="mRNA"	
	/cultivar="B73"	
	/db_xref="taxon:4577"	
	/clones="MEST2-G2"	
JOURNAL COMMENT	/tissue_type="above ground tissues"	
	/dev_stage="two-leaf-stage green seedling"	
	/lab_host="XLI-MFR Blue"	
	/clone_lib="ISUM2"	
JOURNAL COMMENT	/notes="Organ: green seedlings; Vector: PAD-GAL4; Site_1: EcoRI; Site 2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as PAD-GAL4 phagemids."	
	BASE COUNT 149 a 267 c 213 g 178 t 10 others	
	ORIGIN	
JOURNAL COMMENT	Query Match 96.0%; Score 310; DB 9; Length 817;	
	Best Local Similarity 99.4%; Pred. No. 5.4e-61;	
	Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
	QY 1 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 60	
JOURNAL COMMENT	Db 252 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 311	
	QY 61 CAGCAAGGTGGCTTGTGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 120	
	Db 312 CAGCAAGGTGGCTTGTGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 371	
	QY 121 CTACTGGACCATGTGGAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180	
JOURNAL COMMENT	Db 372 CTACTGGACCATGTGGAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 430	
	QY 181 AGGAGCTGCGAGGAGCCATCAATCTCTACCGGACGCTTCCACCGGTCTCG 240	
	Db 431 AGGAGCTGCGAGGAGCCATCAATCTCTACCGGACGCTTCCACCGGTCTCG 490	
	QY 241 ACAACATCAAGCAGACGAGTGGTCACTTCATCGCTACAAGCCCCGGGAGGACT 300	
JOURNAL COMMENT	Db 491 ACAACATCAAGCAGACGAGTGGTCACTTCATCGCTACAAGCCCCGGGAGGACT 550	
	QY 301 AGACCGCGCCCGCGCGCGCC 323	
	Db 551 AGACCGCGCCCGCGCGCGCC 573	

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RESULT 14
BI319103/c
LOCUS
DEFINITION
  BI319103 475 bp mRNA linear EST 23-JUL-2001
  949039D04.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
  Zea mays cDNA, mRNA sequence.
ACCESSION
  BI319103
VERSION
  BI319103.1 GI:14996985
KEYWORDS
  EST.
SOURCE
  Zea mays
  Zea mays
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  Walbot.V.
  Maize ESTs from various cDNA libraries sequenced at Stanford
  University
  Unpublished
  CONTACT: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 949039 row: D column: 04.
  Location/Qualifiers
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    /organism="Zea mays"
    /mol_type="mRNA"
    /cultivar="W64A"
    /db_xref="taxon:4577"
    /tissue_type="immature leaf primordium and vegetative
    meristem"
    /dev_stage="4 stages from 3-13 days after imbibing"
    /lab_host="E. coli XL0LR"
    /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
    Moose"
    /note="Organ: juvenile vegetative shoots; Vector:
    pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
    of total RNA by weight from 4 tissue sources (see below)
    were pooled, polyA+ RNA isolated, and cDNA synthesized for
    EcoRI (5') and XhoI (3') directional cloning into lambda
    Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
    shoots 3 days after sowing/imbibing in wet soil. 2. Basal
    1.5 cm shoots 6 days after sowing - includes yellow
    portions of developing leaves 1-5, primordia from 6-8, and
    the vegetative apex. 3. Non-green portions of developing
    leaves 4-5 and the vegetative apex, including adult leaf
    primordia, 9 days after sowing. 4. Partially expanded and
    greening leaves 4-5 at 13 days after sowing."
BASE COUNT
  110 a 123 c 164 g 78 t
ORIGIN
  Query Match 95.8%; Score 309.4; DB 12; Length 475;
  Best Local Similarity 99.4%; Pred. No. 6.6e-61;
  Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGACTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 60
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D 475 CGACCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 416
  |||||

QY 61 CAGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGAGCGCG 120
  |||||
D 415 CAGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGAGCGCG 356
  |||||

QY 121 CTACTGGACCATGTGGAAGCATGCGGTTCGCAACGCGCCACCGAGGTGTACA 180
  |||||
D 355 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGGTGCAACGCGCCACCGAGGTGTACA 297
  |||||

QY 181 AGGAGCTGCAGGAGGCCATCAATCTCACCAGGAGCGCTTCCACCGCGTCAATCGGCTTCG 240
  |||||
  
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296 AGGAGCTGCAGGAGGCCATCAATCTCACCAGGAGCGCTTCCACCGCGTCAATCGGCTTCG 237
241 ACAACATCAAGCAGCAGCGAGTGGTTCAGCTTTCATCGCTTACAGCCCCCGGGCAGCGACT 300
  |||||
D 236 ACAACATCAAGCAGCAGCGAGTGGTTCAGCTTTCATCGCTTACAGCCCCCGGGCAGCGACT 177
  |||||

QY 301 AGACCGCGCCCGCGCGCGCCCC 323
  |||||
D 176 AGACCGCGCCCGCGCGCGCCCC 154
  |||||

RESULT 15
BE055905
LOCUS
DEFINITION
  BE055905 553 bp mRNA linear EST 08-JUN-2000
  945017B11.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
  (SK) Zea mays cDNA, mRNA sequence.
ACCESSION
  BE055905
VERSION
  BE055905.1 GI:8382962
KEYWORDS
  EST.
SOURCE
  Zea mays
  Zea mays
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  Walbot.V.
  Maize ESTs from various cDNA libraries sequenced at Stanford
  University
  Unpublished
  CONTACT: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 945017 row: B column: 11.
  Location/Qualifiers
    1..553
    /organism="Zea mays"
    /mol_type="mRNA"
    /cultivar="W23"
    /db_xref="taxon:4577"
    /tissue_type="tassel, kernal, silk, husk, root, leaf"
    /dev_stage="fully-grown"
    /lab_host="DH10B"
    /clone_lib="945 - Mixed adult tissues from Walbot lab,
    same as 707 (SK)"
    /note="Organ: tassel, kernal, silk, husk, root, leaf;
    Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
    differentiated maize tissues from an active Mutator plant.
    Tissue ratio is 4:2:1:1:1 (tassel, kernel, silk, husk,
    root, leaf). Unidirectionally cloned. New library number
    given to library 707 for additional sequencing."
BASE COUNT
  101 a 197 c 157 g 98 t
ORIGIN
  Query Match 95.8%; Score 309.4; DB 10; Length 553;
  Best Local Similarity 99.4%; Pred. No. 6.8e-61;
  Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGACTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 60
  |||||
D 138 CGATCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 197
  |||||

QY 61 CAGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGAGCGCG 120
  |||||
D 198 CAGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGAGCGCG 257
  |||||

QY 121 CTACTGGACCATGTGGAAGCATGCGGTTCGCAACGCGCCACCGAGGTGTACA 180
  |||||
D 258 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGGTGCAACGCGCCACCGAGGTGTACA 316
  |||||
  
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Mon Dec 1 12:52:48 2003

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Qy 181 AGGAGCTGCAGGAGGCCATCAAAATCCTACCGGAGCCCTTCCACCGGTCTATCGGCTTCG 240
Db |||||
Qy 317 AGGAGCTGCAGGAGGCCATCAAAATCCTACCGGAGCCCTTCCACCGGTCTATCGGCTTCG 376
Db |||||
Qy 241 ACAACATCAAGCAGACGCGAGTGCCTTTCATCGCCCTACAAGCCCCCGGGCAGCGACT 300
Db |||||
Qy 377 ACAACATCAAGCAGACGCGAGTGCCTTTCATCGCCCTACAAGCCCCCGGGCAGCGACT 436
Db |||||
Qy 301 AGACCGCGCCCGCGCGCGCCCC 323
Db |||||
Qy 437 AGACCGCGCCCGCGCGCGCCCC 459
Db |||||
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